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JUL 31 2001

# Raw Sequence Listing Error Summary

TECH CENTER 1600/2900

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/549,096

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                          (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                          <210> sequence id number  
                          <400> sequence id number  
                          000
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                          Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                          Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                          (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/549,096

DATE: 07/05/2001  
TIME: 16:28:38

Input Set : A:\PTO.txt  
Output Set: N:\CRF3\07032001\I549096.raw

Does Not Comply  
Corrected Diskette Needed

2 <110> APPLICANT: Ware, Carl F.  
4 <120> TITLE OF INVENTION: LIGAND FOR HERPES SIMPLEX VIRUS ENTRY MEDIATOR AND METHODS  
OF USE  
6 <130> FILE REFERENCE: 051501/0276397  
8 <140> CURRENT APPLICATION NUMBER: 09/549,096  
9 <141> CURRENT FILING DATE: 2000-04-12  
11 <160> NUMBER OF SEQ ID NOS: 6  
13 <170> SOFTWARE: PatentIn Ver. 2.0

# ERRORED SEQUENCES

61 <210> SEQ ID NO: 5  
62 <211> LENGTH: 1169  
63 <212> TYPE: DNA  
64 <213> ORGANISM: Homo sapiens  
66 <220> FEATURE:  
67 <221> NAME/KEY: CDS  
68 <222> LOCATION: (49)..(771)  
70 <400> SEQUENCE: 5  
71 gaggttgaag gacccaggcg tgtcagccct gctccagaga ccttgggc atg gag gag 57  
72 Met Glu Glu  
W--> 73  
74 agt gtc gta cgg ccc tca gtg ttt gtg gtg gat gga cag acc gac atc 105  
75 Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln Thr Asp Ile  
W--> 76 5 10 15  
W--> 77 ttc acg agg ctg gga cga agc cac cgg aga cag tcg tgc agt gtg 153  
E--> 78 Phe thr arg Leu gly arg ser his arg arg gln ser cys ser val  
W--> 79 25 30 35  
W--> 80 ggt ctc ttg ctg ttg ctg atg ggg gct ggg ctg 201  
E--> 81 gly Leu Leu Leu Leu Leu met gly ala gly Leu  
E--> 82 45 50  
E--> 83 gcc gtc caa ggc tgg ttc ctc ctg cag ctg cac tgg cgt cta gga gag 249  
84 Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg Leu Gly Glu  
W--> 85 55 60 65  
E--> 86 atg gtc acc cgc ctg cct gac gga cct gca ggc tcc tgg gag cag ctg 297  
87 Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp Glu Gln Leu  
W--> 88 70 75 80  
E--> 89 ata caa gag cga agg tct cac gag gtc aac cca gca gcg cat ctc aca 345  
90 Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala His Leu Thr  
W--> 91 85 90 95  
W--> 92 gcc aac tcc agc ttg acc ggc agc ggg ggg ccg ctg tta tgg gag 393  
E--> 93 ala asn ser ser Leu thr gly ser gly gly Pro Leu Leu trp glu  
W--> 94 105 110 115  
W--> 95 gcc ttc ctg agg ggc ctc agc tac cac gat ggg 441  
W--> 96 Ala Phe Leu Arg Gly Leu Ser Tyr His Asp Gly  
W--> 97 120 125 130  
E--> 98 gcc ctt gtg gtc acc aaa gct ggc tac tac tac atc tac tcc aag gtg 489

DO NOT use  
TAB codes

↓  
move under respective  
codons

cca  
Pro  
20  
gcc cgg gtg ggt ctg  
Ala Arg Val Gly Leu  
40

What is  
this?

initial grouping  
of codons and amino  
acids

ggg  
Gly  
100  
act cag ctg ggc ctg  
Thr Gln Leu Gly Leu

## RAW SEQUENCE LISTING

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Input Set : A:\PTO.txt

Output Set: N:\CRF3\07032001\I549096.raw

*Same  
over*

```

99 Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr Ser Lys Val
W--> 100 135          140          145
E--> 101 cag ctg ggc ggt gtg ggc tgc ccg ctg ggc ctg gcc agc acc atc acc 537
      102 Gln Leu Gly Gly Val Gly Cys Pro Leu Gly Leu Ala Ser Thr Ile Thr
W--> 103 150          155          160          cac ggc
W--> 104 ctc tac aag cgc aca ccc cgc tac ccc gag gag ctg gag ctg 585          His Gly
E--> 105 Leu tyr Lys arg thr Pro arg tyr Pro glu glu Leu glu Leu          165
W--> 106 170          175          ttg gtc agc cag cag tca
W--> 107 ccc tgc gga cgg gcc acc agc agc tcc cgg 633          Leu Val Ser Gln Gln Ser
E--> 108 Pro cys gly arg ala thr ser ser ser arg          180          185
W--> 109 190          195          gtc tgg tgg gac agc agc ttc ctg ggt ggt
W--> 110 gtg gta cac ctg gag gct 681          Val Trp Trp Asp Ser Ser Phe Leu Gly Gly
E--> 111 val val his Leu glu ala          200          205
E--> 112 210
E--> 113 ggg gag gag gtg gtc gtc cgt gtg ctg gat gaa cgc ctg gtt cga ctg 729
      114 Gly Glu Glu Val Val Val Arg Val Leu Asp Glu Arg Leu Val Arg Leu
W--> 115 215          220          225
E--> 116 cgt gat ggt acc cgg tct tac ttc ggg gct ttc atg gtg tga 771
      117 Arg Asp Gly Thr Arg Ser Tyr Phe Gly Ala Phe Met Val
W--> 118 230          235          240
E--> 119 aggaaggagc gtggtgcatt ggacatgggt ctgacacgtg gagaactcag aggggtgcctc 831
E--> 120 aggggaaaga aaactcacga agcagaggct gggcgtggtg gctctcgctt gtaatcccg 891
E--> 121 cactttggga ggccaaggca ggcggatcac ctgaggtcag gagttcgaga ccagcctggc 951
E--> 122 taacatggca aaaccccatc tctactaaaa atacaaaaat tagccggacg tgggtggtgcc 1011
E--> 123 tgcctgtaat ccagctactc aggaggtcga ggcaggataa ttttgcttaa acccgggagg 1071
E--> 124 cggaggttgc agtgagccga gatcacacca ctgcactcca acctgggaaa cgcagtgaga 1131
E--> 125 ctgtgcctca aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1169
127 <210> SEQ ID NO: 6
128 <211> LENGTH: 240
129 <212> TYPE: PRT
130 <213> ORGANISM: Homo sapiens
W--> 131 <400> SEQUENCE: 6
      132 Met Glu Glu Ser Val Val Arg Pro Ser Val Phe Val Val Asp Gly Gln
      133 1 5 10 15
      134 Thr Asp Ile Pro Phe Thr Arg Leu Gly Arg Ser His Arg Arg Gln Ser
E--> 135 20 25 30
      136 Cys Ser Val Ala Arg Val Gly Leu Gly Leu Leu Leu Leu Met Gly
E--> 137 35 40 45
      138 Ala Gly Leu Ala Val Gln Gly Trp Phe Leu Leu Gln Leu His Trp Arg
E--> 139 50 55 60
      140 Gly Glu Met Val Thr Arg Leu Pro Asp Gly Pro Ala Gly Ser Trp
E--> 141 70 75 80
      142 Glu Gln Leu Ile Gln Glu Arg Arg Ser His Glu Val Asn Pro Ala Ala
E--> 143 85 90 95
      144 His Leu Thr Gly Ala Asn Ser Ser Leu Thr Gly Ser Gly Gly Pro Leu
E--> 145 100 105 110
      146 Leu Trp Glu Thr Gln Leu Gly Leu Ala Phe Leu Arg Gly Leu Ser Tyr
E--> 147 115 120 125
      148 Gly Ala Leu Val Val Thr Lys Ala Gly Tyr Tyr Tyr Ile Tyr

```

*misaligned  
amino acid nos.  
(see item 3 on  
Even summary  
sheet)*

Leu  
65

*misaligned  
grouping*

His Asp  
130

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*same  
env*

```

E--> 149 135                               140          Ser Lys Val Gln Leu Gly
      150 Gly Val Gly Cys Pro Leu Gly Leu Ala Ser          145          150
E--> 151 155                               160          Thr Ile Thr His Gly Leu Tyr Lys Arg Thr
      152 Pro Arg Tyr Pro Glu Glu                          165          170
E--> 153 175
      154 Leu Glu Leu Leu Val Ser Gln Gln Ser Pro Cys Gly Arg Ala Thr Ser
E--> 155 180                               185          190
      156 Ser Ser Arg Val Trp Trp Asp Ser Ser Phe Leu Gly Gly Val Val His
E--> 157 195                               200          205
      158 Ala Gly Glu Glu Val Val Arg Val Leu Asp Glu Arg Leu          Leu Glu
E--> 159 215                               220          Val Arg Leu Arg Asp Gly
      160 Thr Arg Ser Tyr Phe Gly Ala Phe Met Val          225          230
E--> 161 235                               240
      163 ATTORNEY DOCKET NO. 07246/030001
E--> 166 2

```

*delete at end of file*

*All sample Sequence Listing  
(attached) for robot format*

*PS* Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001  
<141> 1998-12-31

<150> US 08/999,999  
<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1  
<211> 389  
<212> DNA  
<213> Paramecium sp.

<220>  
<221> CDS  
<222> (279)...(389)

<300>  
<301> Doe, Richard  
<302> Isolation and Characterization of a Gene Encoding a  
Protease from Paramecium sp.  
<303> Journal of Genes  
<304> 1  
<305> 4  
<306> 1-7  
<307> 1988-06-31  
<308> 123456  
<309> 1988-06-31

<400> 1  
agctgtagtc attcctgtgt cctcttctct ctgggcttct caccctgcta atcagatctc 60  
agggagagtg tcttgacctt cctctgcctt tgcagcttca caggcaggca ggcaggcagc 120  
tgatgtggca attgctggca gtgccacagg cttttcagcc aggccttaggg tgggttccgc 180  
cgcgggcgcg cgccccctct cgcgctctct tcgcgcctct ctctcgctct cctctcgctc 240

Appendix 3, page 2

ggacctgatt	aggtgagcag	gaggaggggg	cagtttagc	atg Met 1	gtt Val	tca Ser	atg Met	ttc Phe 5	agc Ser	296						
ttg Leu	tct Ser	ttc Phe	aaa Lys 10	tgg Trp	cct Pro	gga Gly	ttt Phe	tgt Cys 15	ttg Leu	ttt Phe	gtt Val	tgt Cys	ttg Leu 20	ttc Phe	caa Gln	344
tgt Cys	ccc Pro	aaa Lys 25	gtc Val	ctc Leu	ccc Pro	tgt Cys	cac His 30	tca Ser	tca Ser	ctg Leu	cag Gln	ccg Pro 35	aat Asn	ctt Leu	389	

  

<210> 2  
 <211> 37  
 <212> PRT  
 <213> Paramecium sp.

  

<400> 2  
 Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu  
 1 5 10 15

Phe Val Cys Leu Phe Gln Cys Pro Lys Val Leu Pro Cys His Ser Ser  
 20 25 30

Leu Gln Pro Asn Leu  
 35

  

<210> 3  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

  

<220>  
 <223> Designed peptide based on size and polarity to act as a  
 linker between the alpha and beta chains of Protein XYZ.

  

<400> 3  
 Met Val Asn Leu Glu Pro Met His Thr Glu Ile  
 1 5 10

  

<210> 4  
 <400> 4  
 000

[Annex VIII follows]

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO: #:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified



		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0
<302>	Title		0
<303>	Journal		0
<304>	Volume		0
<305>	Issue		0
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	0
<308>	Database Accession Number	Accession number assigned by database including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	0
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	0

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	M

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(c) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;

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Input Set : A:\PTO.txt

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:73 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:76 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4  
 L:77 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:77 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16  
 L:78 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
 L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
 L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:78 M:254 E: No. of Bases conflict, LENGTH:Input:20 Counted:150 SEQ:5  
 L:78 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
 L:78 M:112 C: (48) String data converted to lower case,  
 L:79 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8  
 L:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:80 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:12  
 L:81 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 M:254 Repeated in SeqNo=5  
 L:81 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17  
 M:112 Repeated in SeqNo=5  
 L:85 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:91 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4  
 L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:92 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:16  
 L:93 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
 L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
 L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:93 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:17  
 L:94 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8  
 L:95 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:95 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:12  
 L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:97 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:100 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:103 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5  
 L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:104 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:15  
 L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:105 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14  
 L:106 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8  
 L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:107 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11  
 L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
 L:108 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7  
 L:109 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:12  
 L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/549,096

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Input Set : A:\PTO.txt

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L:110 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:111 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7  
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5  
L:125 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1169 Found:1046 SEQ:5  
L:131 M:283 W: Missing Blank Line separator, <400> field identifier  
L:135 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6  
M:332 Repeated in SeqNo=6  
L:139 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:166 M:252 E: No. of Seq. differs, <211>LENGTH:Input:240 Found:171 SEQ:6